



SEQUENCE LISTING

<110> Kumar, Rajesh
Sahni, Girish
Roy, Chait
Rajagopal, Kammara
Nihalani, Deepak
Sundaram, Vasudha
Yadav, Mahavir

<120> NOVEL CLOT-SPECIFIC STREPTOKINASE
PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
PROTEIN

<130> 07064-009002

<140> 09/940,235

<141> 2001-08-27

<150> 09/471,349

<151> 1999-12-23

<150> IN 3825/DEL/98

<151> 1998-12-24

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1245

<212> DNA

<213> Streptococcus equisimilis

<220>

<221> CDS

<222> (1)...(1242)

<400> 1

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Ile Ala Gly Pro Glu Trp Leu Leu Asp Arg Pro Ser Val Asn Asn Ser	
1 5 10 15	

caa tta gtt gtt agc gtt gct ggt act gtt gag ggg acg aat caa gac	96
Gln Leu Val Val Ser Val Ala Gly Thr Val Glu Gly Thr Asn Gln Asp	
20 25 30	

att agt ctt aaa ttt ttt gaa atc gat cta aca tca cga cct gct cat	144
Ile Ser Leu Lys Phe Phe Glu Ile Asp Leu Thr Ser Arg Pro Ala His	
35 40 45	

gga gga aag aca gag caa ggc tta agt cca aaa tca aaa cca ttt gct	192
Gly Gly Lys Thr Glu Gln Gly Leu Ser Pro Lys Ser Lys Pro Phe Ala	
50 55 60	

act gat agt ggc gcg atg tca cat aaa ctt gag aaa gct gac tta cta	240
Thr Asp Ser Gly Ala Met Ser His Lys Leu Glu Lys Ala Asp Leu Leu	
65 70 75 80	
aag gct att caa gaa caa ttg atc gct aac gtc cac agt aac gac gac	288
Lys Ala Ile Gln Glu Gln Leu Ile Ala Asn Val His Ser Asn Asp Asp	
85 90 95	
tac ttt gag gtc att gat ttt gca agc gat gca acc att act gat cga	336
Tyr Phe Glu Val Ile Asp Phe Ala Ser Asp Ala Thr Ile Thr Asp Arg	
100 105 110	
aac ggc aag gtc tac ttt gct gac aaa gat ggt tcg gta acc ttg ccg	384
Asn Gly Lys Val Tyr Phe Ala Asp Lys Asp Gly Ser Val Thr Leu Pro	
115 120 125	
acc caa cct gtc caa gaa ttt ttg cta agc gga cat gtg cgc gtt aga	432
Thr Gln Pro Val Gln Glu Phe Leu Leu Ser Gly His Val Arg Val Arg	
130 135 140	
cca tat aaa gaa aaa cca ata caa aac caa gcg aaa tct gtt gat gtg	480
Pro Tyr Lys Glu Lys Pro Ile Gln Asn Gln Ala Lys Ser Val Asp Val	
145 150 155 160	
gaa tat act gta cag ttt act ccc tta aac cct gat gac gat ttc aga	528
Glu Tyr Thr Val Gln Phe Thr Pro Leu Asn Pro Asp Asp Asp Phe Arg	
165 170 175	
cca ggt ctc aaa gat act aag cta ttg aaa aca cta gct atc ggt gac	576
Pro Gly Leu Lys Asp Thr Lys Leu Leu Lys Thr Leu Ala Ile Gly Asp	
180 185 190	
acc atc aca tct caa gaa tta cta gct caa gca caa agc att tta aac	624
Thr Ile Thr Ser Gln Glu Leu Leu Ala Gln Ala Gln Ser Ile Leu Asn	
195 200 205	
aaa aac cac cca ggc tat acg att tat gaa cgt gac tcc tca atc gtc	672
Lys Asn His Pro Gly Tyr Thr Ile Tyr Glu Arg Asp Ser Ser Ile Val	
210 215 220	
act cat gac aat gac att ttc cgt acg att tta cca atg gat caa gag	720
Thr His Asp Asn Asp Ile Phe Arg Thr Ile Leu Pro Met Asp Gln Glu	
225 230 235 240	
ttt act tac cgt gtt aaa aat cgg gaa caa gct tat agg atc aat aaa	768
Phe Thr Tyr Arg Val Lys Asn Arg Glu Gln Ala Tyr Arg Ile Asn Lys	
245 250 255	
aaa tct ggt ctg aat gaa gaa ata aac aac act gac ctg atc tct gag	816
Lys Ser Gly Leu Asn Glu Glu Ile Asn Asn Thr Asp Leu Ile Ser Glu	
260 265 270	
aaa tat tac gtc ctt aaa aaa ggg gaa aag ccg tat gat ccc ttt gat	864
Lys Tyr Tyr Val Leu Lys Lys Gly Glu Lys Pro Tyr Asp Pro Phe Asp	
275 280 285	

cgc agt cac ttg aaa ctg ttc acc atc aaa tac gtt gat gtc gat acc 912
 Arg Ser His Leu Lys Leu Phe Thr Ile Lys Tyr Val Asp Val Asp Thr
 290 295 300

 aac gaa ttg cta aaa agt gag cag ctc tta aca gct agc gaa cgt aac 960
 Asn Glu Leu Leu Lys Ser Glu Gln Leu Leu Thr Ala Ser Glu Arg Asn
 305 310 315 320

 tta gac ttc aga gat tta tac gat cct cgt gat aag gct aaa cta ctc 1008
 Leu Asp Phe Arg Asp Leu Tyr Asp Pro Arg Asp Lys Ala Lys Leu Leu
 325 330 335

 tac aac aat ctc gat gct ttt ggt att atg gac tat acc tta act gga 1056
 Tyr Asn Asn Leu Asp Ala Phe Gly Ile Met Asp Tyr Thr Leu Thr Gly
 340 345 350

 aaa gta gag gat aat cac gat gac acc aac cgt atc ata acc gtt tat 1104
 Lys Val Glu Asp Asn His Asp Asp Thr Asn Arg Ile Ile Thr Val Tyr
 355 360 365

 atg ggc aag cga ccc gaa gga gag aat gct agc tat cat tta gcc tat 1152
 Met Gly Lys Arg Pro Glu Gly Glu Asn Ala Ser Tyr His Leu Ala Tyr
 370 375 380

 gat aaa gat cgt tat acc gaa gaa gaa cga gaa gtt tac agc tac ctg 1200
 Asp Lys Asp Arg Tyr Thr Glu Glu Glu Arg Glu Val Tyr Ser Tyr Leu
 385 390 395 400

 cgt tat aca ggg aca cct ata cct gat aac cct aac gac aaa 1242
 Arg Tyr Thr Gly Thr Pro Ile Pro Asp Asn Pro Asn Asp Lys
 405 410

 taa 1245

<210> 2
 <211> 414
 <212> PRT
 <213> Streptococcus equisimilis

<400> 2
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 Gln Leu Val Val Ser Val Ala Gly Thr Val Glu Gly Thr Asn Gln Asp
 20 25 30
 Ile Ser Leu Lys Phe Phe Glu Ile Asp Leu Thr Ser Arg Pro Ala His
 35 40 45
 Gly Gly Lys Thr Glu Gln Gly Leu Ser Pro Lys Ser Lys Pro Phe Ala
 50 55 60
 Thr Asp Ser Gly Ala Met Ser His Lys Leu Glu Lys Ala Asp Leu Leu
 65 70 75 80
 Lys Ala Ile Gln Glu Gln Leu Ile Ala Asn Val His Ser Asn Asp Asp
 85 90 95
 Tyr Phe Glu Val Ile Asp Phe Ala Ser Asp Ala Thr Ile Thr Asp Arg
 100 105 110
 Asn Gly Lys Val Tyr Phe Ala Asp Lys Asp Gly Ser Val Thr Leu Pro
 115 120 125
 Thr Gln Pro Val Gln Glu Phe Leu Leu Ser Gly His Val Arg Val Arg

130		135		140
Pro Tyr Lys Glu Lys	Pro Ile Gln Asn Gln	Ala Lys Ser Val Asp Val		
145	150	155		160
Glu Tyr Thr Val Gln	Phe Thr Pro Leu Asn	Pro Asp Asp Asp Phe Arg		
	165	170		175
Pro Gly Leu Lys Asp	Thr Lys Leu Leu Lys	Thr Leu Ala Ile Gly Asp		
	180	185		190
Thr Ile Thr Ser Gln	Glu Leu Leu Ala Gln	Ala Gln Ser Ile Leu Asn		
	195	200		205
Lys Asn His Pro Gly	Tyr Thr Ile Tyr Glu	Arg Asp Ser Ser Ile Val		
210	215	220		
Thr His Asp Asn Asp	Ile Phe Arg Thr Ile	Leu Pro Met Asp Gln Glu		
225	230	235		240
Phe Thr Tyr Arg Val	Lys Asn Arg Glu Gln	Ala Tyr Arg Ile Asn Lys		
	245	250		255
Lys Ser Gly Leu Asn	Glu Glu Ile Asn Asn	Thr Asp Leu Ile Ser Glu		
	260	265		270
Lys Tyr Tyr Val Leu	Lys Lys Gly Glu Lys	Pro Tyr Asp Pro Phe Asp		
	275	280		285
Arg Ser His Leu Lys	Leu Phe Thr Ile Lys	Tyr Val Asp Val Asp Thr		
290	295	300		
Asn Glu Leu Leu Lys	Ser Glu Gln Leu Leu	Thr Ala Ser Glu Arg Asn		
305	310	315		320
Leu Asp Phe Arg Asp	Leu Tyr Asp Pro Arg	Asp Lys Ala Lys Leu Leu		
	325	330		335
Tyr Asn Asn Leu Asp	Ala Phe Gly Ile Met	Asp Tyr Thr Leu Thr Gly		
	340	345		350
Lys Val Glu Asp Asn	His Asp Asp Thr Asn	Arg Ile Ile Thr Val Tyr		
	355	360		365
Met Gly Lys Arg Pro	Glu Gly Glu Asn Ala	Ser Tyr His Leu Ala Tyr		
370	375	380		
Asp Lys Asp Arg Tyr	Thr Glu Glu Glu Arg	Glu Val Tyr Ser Tyr Leu		
385	390	395		400
Arg Tyr Thr Gly Thr	Pro Ile Pro Asp Asn	Pro Asn Asp Lys		
	405	410		

<210> 3
 <211> 777
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(777)

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Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln		
1 5 10 15		
agc aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa		96
Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln		
20 25 30		
cag tgg gag cgg acc tac cta ggt aat gtg ttg gtt tgt act tgt tat		144
Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys Thr Cys Tyr		
35 40 45		

gga gga agc cga ggt ttt aac tgc gaa agt aaa cct gaa gct gaa gag Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu 50 55 60	192
act tgc ttt gac aag tac act ggg aac act tac cga gtg ggt gac act Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr 65 70 75 80	240
tat gag cgt cct aaa gac tcc atg atc tgg gac tgt acc tgc atc ggg Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly 85 90 95	288
gct ggg cga ggg aga ata agc tgt acc atc gca aac cgc tgc cat gaa Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu 100 105 110	336
ggg ggt cag tcc tac aag att ggt gac acc tgg agg aga cca cat gag Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu 115 120 125	384
act ggt ggt tac atg tta gag tgt gtg tgt ctt ggt aat gga aaa gga Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly 130 135 140	432
gaa tgg acc tgc aag ccc ata gct gag aag tgt ttt gat cat gct gct Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala 145 150 155 160	480
ggg act tcc tat gtg gtc gga gaa acg tgg gag aag ccc tac caa ggc Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly 165 170 175	528
tgg atg atg gta gat tgt act tgc ctg gga gaa ggc agc gga cgc atc Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile 180 185 190	576
act tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser 195 200 205	624
tat aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu 210 215 220	672
ctc cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu 225 230 235 240	720
agg cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr 245 250 255	768
gat gtt cgt Asp Val Arg	777

<210> 4
 <211> 259
 <212> PRT
 <213> Homo sapiens

<400> 4
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 1 5 10 15
 Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln
 20 25 30
 Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys Thr Cys Tyr
 35 40 45
 Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu
 50 55 60
 Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr
 65 70 75 80
 Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly
 85 90 95
 Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu
 100 105 110
 Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu
 115 120 125
 Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly
 130 135 140
 Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala
 145 150 155 160
 Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly
 165 170 175
 Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile
 180 185 190
 Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser
 195 200 205
 Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu
 210 215 220
 Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu
 225 230 235 240
 Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr
 245 250 255
 Asp Val Arg

<210> 5
 <211> 1377
 <212> DNA
 <213> Streptococcus equisimilis

<400> 5
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 agatatacca tgattgctgg acctgagtgg ctgctagacc gtccatctgt caacaacagc 180
 caattgggtt ttagcggtgc tgggtactgt gaggggacga atcaagacat tagtcttaaa 240
 ttttttgaaa tcgatctaac atcacgacct gctcatggag gaaagacaga gcaaggctta 300
 agtccaaaat caaaaccatt tgctactgat agtggcgcgca tgtcacataa acttgagaaa 360
 gctgacttac taaaggctat tcaagaacaa ttgatcgcta acgtccacag taacgacgac 420
 tactttgagg tcattgattt tgcaagcgat gcaaccatta ctgatcgaaa cggcaaggtc 480
 tactttgctg acaaagatgg ttcggttaacc ttgccgaccc aacctgtcca agaatttttg 540

ctaagcggac	atgtgcgcg	tagaccatat	aaagaaaaac	caatacaaaa	ccaagcgaaa	600
tctgttgatg	tggaatatac	tgtacagttt	actcccttaa	accctgatga	cgatttcaga	660
ccaggtctca	aagatactaa	gctattgaaa	acactagcta	tcggtgacac	catcacatct	720
caagaattac	tagctcaagc	acaaagcatt	ttaaacaana	accacccagg	ctatacgatt	780
tatgaacgtg	actcctcaat	cgtaactcat	gacaatgaca	ttttccgtac	gattttacca	840
atggatcaag	agtttactta	ccgtgttaaa	aatcggaac	aagcttatag	gatcaataaa	900
aaatctggtc	tgaatgaaga	aataaacaac	actgacctga	tctctgagaa	atattacgtc	960
cttaaaaaag	gggaaaagcc	gtatgatccc	tttgatcgca	gtcacttgaa	actgttcacc	1020
atcaaatacg	ttgatgtcga	taccaacgaa	ttgctaaaaa	gtgagcagct	cttaacagct	1080
agcgaacgta	acttagactt	cagagattta	tacgatcctc	gtgataaggc	taaactactc	1140
tacaacaatc	tcgatgcttt	tggtattatg	gactatacct	taactggaaa	agtagaggat	1200
aatcacgatg	acaccaaccg	tatcataacc	gtttatatgg	gcaagcgacc	cgaaggagag	1260
aatgctagct	atcatttagc	ctatgataaa	gatcgttata	ccgaagaaga	acgagaagtt	1320
tacagctacc	tgcgtttatac	agggacacct	atacctgata	accctaacga	caaataa	1377

<210> 6

<211> 1327

<212> DNA

<213> Streptococcus equisimilis

<400> 6

taatacgact	cactataggg	agaccacaac	ggtttccctc	tagaaataat	tttgtttaac	60
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aaataacagc	caattgggtg	ttagcggttg	tggtactgtt	gaggggacga	atcaagacat	180
tagtcttaaa	ttttttgaaa	tcgatctaac	atcacgacct	gctcatggag	gaaagacaga	240
gcaaggctta	agtccaaaat	caaaaccatt	tgctactgat	agtggcgcca	tgtaacataa	300
acttgagaaa	gctgacttac	taaaaggctat	tcaagaacaa	ttgatcgcta	acgtccacag	360
taacgacgac	tactttgagg	tcattgattt	tgcaagcgat	gcaaccatta	ctgatcgaaa	420
cggaagggtc	tactttgctg	acaaagatgg	ttcggttaacc	ttgccgaccc	aacctgtcca	480
agaatttttg	ctaagcggac	atgtgcgcg	tagaccatat	aaagaaaaac	caatacaaaa	540
ccaagcgaaa	tctgttgatg	tggaatatac	tgtacagttt	actcccttaa	accctgatga	600
cgatttcaga	ccaggtctca	aagatactaa	gctattgaaa	acactagcta	tcggtgacac	660
catcacatct	caagaattac	tagctcaagc	acaaagcatt	ttaaacaana	accacccagg	720
ctatacgatt	tatgaacgtg	actcctcaat	cgtaactcat	gacaatgaca	ttttccgtac	780
gattttacca	atggatcaag	agtttactta	ccgtgttaaa	aatcggaac	aagcttatag	840
gatcaataaa	aaatctggtc	tgaatgaaga	aataaacaac	actgacctga	tctctgagaa	900
atattacgtc	cttaaaaaag	gggaaaagcc	gtatgatccc	tttgatcgca	gtcacttgaa	960
actgttcacc	atcaaatacg	ttgatgtcga	taccaacgaa	ttgctaaaaa	gtgagcagct	1020
cttaacagct	agcgaacgta	acttagactt	cagagattta	tacgatcctc	gtgataaggc	1080
taaactactc	tacaacaatc	tcgatgcttt	tggtattatg	gactatacct	taactggaaa	1140
agtagaggat	aatcacgatg	acaccaaccg	tatcataacc	gtttatatgg	gcaagcgacc	1200
cgaaggagag	aatgctagct	atcatttagc	ctatgataaa	gatcgttata	ccgaagaaga	1260
acgagaagtt	tacagctacc	tgcgtttatac	agggacacct	atacctgata	accctaacga	1320
caaataa						1377

<210> 7

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric gene

<221> CDS

<222> (2)...(49)

<400> 7

g aat gct agc tac cat tta gct ggt ggt ggc cag gcg caa cag att gta 49
 Asn Ala Ser Tyr His Leu Ala Gly Gly Gly Gln Ala Gln Gln Ile Val
 1 5 10 15

ccc 52

<210> 8
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chimeric peptide

<400> 8
 Asn Ala Ser Tyr His Leu Ala Gly Gly Gly Gln Ala Gln Gln Ile Val
 1 5 10 15

<210> 9
 <211> 1541
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Hybrid cassette

<400> 9
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 gtccttctgt aaataacagc caattggttg ttagcggttg tggtagctgt gaggggacga 120
 atcaagacat tagtcttaaa ttttttgaaa tcgatctaac atcacgacct gctcatggag 180
 gaaagacaga gcaaggctta agtccaaaat caaaaccatt tgctactgat agtggcgcgga 240
 tgtcacataa acttgagaaa gctgacttac taaaggctat tcaagaacaa ttgatcgcta 300
 acgtccacag taacgacgac tactttgagg tcattgattt tgcaagcgat gcaaccatta 360
 ctgatcgaaa cggcaagggtc tactttgctg acaaagatgg ttcggtaacc ttgccgaccc 420
 aacctgtcca agaatttttg ctaagcggac atgtgcgcggt tagaccatat aaagaaaaac 480
 caatacaaaa ccaagcgaaa tctgttgatg tggaaatatac tgtacagttt actcccttaa 540
 accctgatga cgatttcaga ccaggctctca aagatactaa gctattgaaa aactagctta 600
 tcggtgacac catcacatct caagaattac tagctcaagc acaaagcatt ttaaacaacaa 660
 accaccaggg ctatacgatt tatgaacgtg actcctcaat cgtcactcat gacaatgaca 720
 ttttccgtac gattttacca atggatcaag agtttactta ccgtgttaaa aatcggggaac 780
 aagcttatag gatcaataaa aaatctggtc tgaatgaaga aataaacaac actgacctga 840
 tctctgagaa atattacgtc cttaaaaaag gggaaaagcc gtatgatccc ttgatcgca 900
 gtcacttgaa actgttcacc atcaaatacg ttgatgtcga taccaacgaa ttgctaaaaa 960
 gtgagcagct cttaacagct agcgaacgta acttagactt cagagattta tacgatcctc 1020
 gtgataaggc taaactactc tacaacaatc tcgatgcttt tggattatg gactataacct 1080
 taactggaaa agtagaggat aatcacgatg acaccaaccg tatcataacc gtttatatgg 1140
 gcaagcgacc cgaaggagag aatgctagct accatttagc tggtaggtggc caggcgcaac 1200
 agattgtacc catagctgag aagtgttttg atcatgctgc tgggacttcc tatgtggtcg 1260
 gagaaacgtg ggagaagccc taccaaggct ggatgatggg agattgtact tgccctgggag 1320
 aaggcagcgg acgcatcact tgcacttcta gaaatagatg caacgatcag gacacaagga 1380
 catcctatag aattggagac acctggagca agaaggataa tcgaggaaac ctgctccagt 1440
 gcatctgcac aggcaacggc cgaggagagt ggaagtgtga gaggcacacc tctgtgcaga 1500
 ccacatcgag cggatctggc cccttcaccg atgttcgtta g 1541

<210> 10
 <211> 1661
 <212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid cassette

<400> 10

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ccaggaccca	acgctgccc	agatctcgat	cccgcgaaat	taatacgact	cactataggg	120
agaccacaac	ggtttccctc	tagaaataat	tttgtttaac	tttaagaagg	agatatacca	180
tgattgctgg	acctgagtgg	ctgctagacc	gtccatctgt	caacaacagc	caattgggtg	240
ttagcgttgc	tggtactgtt	gaggggacga	atcaagacat	tagtcttaaa	ttttttgaaa	300
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caaaaccatt	tgctactgat	agtggcgcg	tgtcacataa	acttgagaaa	gctgacttac	420
taaaggctat	tcaagaacaa	ttgatcgcta	acgtccacag	taacgacgac	tactttgagg	480
tcattgattt	tgcaagcgat	gcaaccatta	ctgatcgaaa	cggaagggtc	tactttgctg	540
acaaagatgg	ttcggtaacc	ttgccgaccc	aacctgtcca	agaatttttg	ctaagcggac	600
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tggaatatac	tgtacagttt	actcccttaa	accctgatga	cgatttcaga	ccagggtctca	720
aagatactaa	gctattgaaa	acactagcta	tcggtgacac	catcacatct	caagaattac	780
tagctcaagc	acaaagcatt	ttaaacaaaa	accacccagg	ctatacgatt	tatgaacgtg	840
actcctcaat	cgtcactcat	gacaatgaca	ttttccgtac	gattttacca	atggatcaag	900
agtttactta	ccgtgttaaa	aatcggaac	aagcttatag	gatcaataaa	aaatctggtc	960
tgaatgaaga	aataaacaac	actgacctga	tctctgagaa	atattacgtc	cttaaaaaag	1020
gggaaaagcc	gtatgatccc	tttgatcgca	gtcacttgaa	actgttcacc	atcaaatacg	1080
ttgatgtcga	taccaacgaa	ttgctaaaaa	gtgagcagct	cttaacagct	agcgaacgta	1140
acttagactt	cagagattta	tacgatcctc	gtgataaggc	taaactactc	tacaacaatc	1200
tcgatgcttt	tggtattatg	gactatacct	taactggaaa	agtagaggat	aatcacgatg	1260
acaccaaccg	tatcataacc	gtttatatgg	gcaagcgacc	cgaaggagag	aatgctagct	1320
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gggagcggac	ctacctaggt	aatgtgttgg	tttgtaactt	ttatggagga	agccgaggtt	1500
ttaactgcga	aagtaaacct	gaagctgaag	agacttgctt	tgacaagtac	actgggaaca	1560
cttaccgagt	gggtgacact	tatgagcgct	ctaaagactc	catgatctgg	gactgtacct	1620
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<211> 1782

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<213> Artificial Sequence

<220>

<223> Hybrid cassette

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ctaacatcac	gacctgctca	tggaggaaa	acagagcaag	gcttaagtcc	aaaatcaaaa	720
ccatttgcta	ctgatagtgg	cgcgatgtca	cataaacttg	agaaagctga	cttactaaag	780

gctattcaag	aacaattgat	cgctaacgtc	cacagtaacg	acgactactt	tgaggtcatt	840
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ttagcctatg	ataaagatcg	ttataccgaa	gaagaacgag	aagtttacag	ctacctgcgt	1740
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<210> 12

<211> 2096

<212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid cassette

<400> 12

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agatctcgat	cccgcgaaat	taatacgact	cactataggg	agaccacaac	ggtttccttc	240
tagaaataat	tttgtttaac	tttaagaagg	agatatacca	tggtgcaagc	acaacagatt	300
gtacccatag	ctgagaagtg	ttttgatcat	gctgctggga	cttcctatgt	ggtcggagaa	360
acgtggggaga	aggcagcgga	cgcatcactt	gcacttctag	aaatagatgc	aacgatcagg	420
acacaaggac	atcctataga	attggagaca	cctggagcaa	gaaggataat	cgaggaaacc	480
tgctccagtg	catctgcaca	ggcaacggcc	gaggagagtg	gaagtgtgag	aggcacacct	540
ctgtgcagac	cacatcgagc	ggatctggcc	ccttcaccga	tgctcgtatt	gctggacctg	600
agtggctgct	agaccgtcca	tctgtcaaca	acagccaatt	ggttgtttagc	gttgctggta	660
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acgaattgct	aaaaagtgag	cagctcttaa	cagctagcga	acgtaactta	gacttcagag	1560
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cttcctatgt	ggtcggagaa	acgtgggaga	agccctacca	aggctggatg	atggtagatt	1860
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atcaggacac	aaggacatcc	tatagaattg	gagacacctg	gagcaagaag	gataatcgag	1980
gaaacctgct	ccagtgcac	tgcacaggca	acggccgagg	agagtggaag	tgtgagaggc	2040
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<211> 53

<212> DNA

<213> Artificial Sequence

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<210> 15

<211> 25

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<212> DNA

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<210> 27
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<210> 28
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<400> 28

atgatagctg gtctgaatgc tactagatcg tccttctgta aat

43

SEQUENCE LISTING

<110> Sahni, Girish
 Kumar, Rajesh
 Roy, Chaiti
 Rajagopal, Kammara
 Nihalani, Deepak
 Sundaram, Vasudha
 Yadav, Mahavir

<120> NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED
 PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
 PREPARATION OF SAID PROTEINS

<130> 07064/009001

<140> US 09/471,349
 <141> 1999-12-23

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caa tta gtt gtt agc gtt gct ggt act gtt gag ggg acg aat caa gac	96
Gln Leu Val Val Ser Val Ala Gly Thr Val Glu Gly Thr Asn Gln Asp	
20 25 30	
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Ile Ser Leu Lys Phe Phe Glu Ile Asp Leu Thr Ser Arg Pro Ala His	
35 40 45	
gga gga aag aca gag caa ggc tta agt cca aaa tca aaa cca ttt gct	192
Gly Gly Lys Thr Glu Gln Gly Leu Ser Pro Lys Ser Lys Pro Phe Ala	
50 55 60	
act gat agt ggc gcg atg tca cat aaa ctt gag aaa gct gac tta cta	240
Thr Asp Ser Gly Ala Met Ser His Lys Leu Glu Lys Ala Asp Leu Leu	
65 70 75 80	

aag gct att caa gaa caa ttg atc gct aac gtc cac agt aac gac gac Lys Ala Ile Gln Glu Gln Leu Ile Ala Asn Val His Ser Asn Asp Asp	288
85 90 95	
tac ttt gag gtc att gat ttt gca agc gat gca acc att act gat cga Tyr Phe Glu Val Ile Asp Phe Ala Ser Asp Ala Thr Ile Thr Asp Arg	336
100 105 110	
aac ggc aag gtc tac ttt gct gac aaa gat ggt tcg gta acc ttg ccg Asn Gly Lys Val Tyr Phe Ala Asp Lys Asp Gly Ser Val Thr Leu Pro	384
115 120 125	
acc caa cct gtc caa gaa ttt ttg cta agc gga cat gtg cgc gtt aga Thr Gln Pro Val Gln Glu Phe Leu Leu Ser Gly His Val Arg Val Arg	432
130 135 140	
cca tat aaa gaa aaa cca ata caa aac caa gcg aaa tct gtt gat gtg Pro Tyr Lys Glu Lys Pro Ile Gln Asn Gln Ala Lys Ser Val Asp Val	480
145 150 155 160	
gaa tat act gta cag ttt act ccc tta aac cct gat gac gat ttc aga Glu Tyr Thr Val Gln Phe Thr Pro Leu Asn Pro Asp Asp Asp Phe Arg	528
165 170 175	
cca ggt ctc aaa gat act aag cta ttg aaa aca cta gct atc ggt gac Pro Gly Leu Lys Asp Thr Lys Leu Leu Lys Thr Leu Ala Ile Gly Asp	576
180 185 190	
acc atc aca tct caa gaa tta cta gct caa gca caa agc att tta aac Thr Ile Thr Ser Gln Glu Leu Leu Ala Gln Ala Gln Ser Ile Leu Asn	624
195 200 205	
aaa aac cac cca ggc tat acg att tat gaa cgt gac tcc tca atc gtc Lys Asn His Pro Gly Tyr Thr Ile Tyr Glu Arg Asp Ser Ser Ile Val	672
210 215 220	
act cat gac aat gac att ttc cgt acg att tta cca atg gat caa gag Thr His Asp Asn Asp Ile Phe Arg Thr Ile Leu Pro Met Asp Gln Glu	720
225 230 235 240	
ttt act tac cgt gtt aaa aat cgg gaa caa gct tat agg atc aat aaa Phe Thr Tyr Arg Val Lys Asn Arg Glu Gln Ala Tyr Arg Ile Asn Lys	768
245 250 255	
aaa tct ggt ctg aat gaa gaa ata aac aac act gac ctg atc tct gag Lys Ser Gly Leu Asn Glu Glu Ile Asn Asn Thr Asp Leu Ile Ser Glu	816
260 265 270	
aaa tat tac gtc ctt aaa aaa ggg gaa aag ccg tat gat ccc ttt gat Lys Tyr Tyr Val Leu Lys Lys Gly Glu Lys Pro Tyr Asp Pro Phe Asp	864
275 280 285	
cgc agt cac ttg aaa ctg ttc acc atc aaa tac gtt gat gtc gat acc Arg Ser His Leu Lys Leu Phe Thr Ile Lys Tyr Val Asp Val Asp Thr	912
290 295 300	
aac gaa ttg cta aaa agt gag cag ctc tta aca gct agc gaa cgt aac	960

Asn	Glu	Leu	Leu	Lys	Ser	Glu	Gln	Leu	Leu	Thr	Ala	Ser	Glu	Arg	Asn			
305					310					315					320			
tta	gac	ttc	aga	gat	tta	tac	gat	cct	cgt	gat	aag	gct	aaa	cta	ctc			1008
Leu	Asp	Phe	Arg	Asp	Leu	Tyr	Asp	Pro	Arg	Asp	Lys	Ala	Lys	Leu	Leu			
				325					330					335				
tac	aac	aat	ctc	gat	gct	ttt	ggt	att	atg	gac	tat	acc	tta	act	gga			1056
Tyr	Asn	Asn	Leu	Asp	Ala	Phe	Gly	Ile	Met	Asp	Tyr	Thr	Leu	Thr	Gly			
			340					345					350					
aaa	gta	gag	gat	aat	cac	gat	gac	acc	aac	cgt	atc	ata	acc	gtt	tat			1104
Lys	Val	Glu	Asp	Asn	His	Asp	Asp	Thr	Asn	Arg	Ile	Ile	Thr	Val	Tyr			
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atg	ggc	aag	cga	ccc	gaa	gga	gag	aat	gct	agc	tat	cat	tta	gcc	tat			1152
Met	Gly	Lys	Arg	Pro	Glu	Gly	Glu	Asn	Ala	Ser	Tyr	His	Leu	Ala	Tyr			
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Asp	Lys	Asp	Arg	Tyr	Thr	Glu	Glu	Glu	Arg	Glu	Val	Tyr	Ser	Tyr	Leu			
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cgt	tat	aca	ggg	aca	cct	ata	cct	gat	aac	cct	aac	gac	aaa					1242
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taa																		1245
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			20					25					30					
Ile	Ser	Leu	Lys	Phe	Phe	Glu	Ile	Asp	Leu	Thr	Ser	Arg	Pro	Ala	His			
		35				40						45						
Gly	Gly	Lys	Thr	Glu	Gln	Gly	Leu	Ser	Pro	Lys	Ser	Lys	Pro	Phe	Ala			
	50					55				60								
Thr	Asp	Ser	Gly	Ala	Met	Ser	His	Lys	Leu	Glu	Lys	Ala	Asp	Leu	Leu			
	65				70					75					80			
Lys	Ala	Ile	Gln	Glu	Gln	Leu	Ile	Ala	Asn	Val	His	Ser	Asn	Asp	Asp			
			85					90					95					
Tyr	Phe	Glu	Val	Ile	Asp	Phe	Ala	Ser	Asp	Ala	Thr	Ile	Thr	Asp	Arg			
		100						105					110					
Asn	Gly	Lys	Val	Tyr	Phe	Ala	Asp	Lys	Asp	Gly	Ser	Val	Thr	Leu	Pro			
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Thr	Gln	Pro	Val	Gln	Glu	Phe	Leu	Leu	Ser	Gly	His	Val	Arg	Val	Arg			
	130					135					140							
Pro	Tyr	Lys	Glu	Lys	Pro	Ile	Gln	Asn	Gln	Ala	Lys	Ser	Val	Asp	Val			
	145				150					155					160			
Glu	Tyr	Thr	Val	Gln	Phe	Thr	Pro	Leu	Asn	Pro	Asp	Asp	Asp	Phe	Arg			
			165					170						175				

Pro Gly Leu Lys Asp Thr Lys Leu Leu Lys Thr Leu Ala Ile Gly Asp
 180 185 190
 Thr Ile Thr Ser Gln Glu Leu Leu Ala Gln Ala Gln Ser Ile Leu Asn
 195 200 205
 Lys Asn His Pro Gly Tyr Thr Ile Tyr Glu Arg Asp Ser Ser Ile Val
 210 215 220
 Thr His Asp Asn Asp Ile Phe Arg Thr Ile Leu Pro Met Asp Gln Glu
 225 230 235 240
 Phe Thr Tyr Arg Val Lys Asn Arg Glu Gln Ala Tyr Arg Ile Asn Lys
 245 250 255
 Lys Ser Gly Leu Asn Glu Glu Ile Asn Asn Thr Asp Leu Ile Ser Glu
 260 265 270
 Lys Tyr Tyr Val Leu Lys Lys Gly Glu Lys Pro Tyr Asp Pro Phe Asp
 275 280 285
 Arg Ser His Leu Lys Leu Phe Thr Ile Lys Tyr Val Asp Val Asp Thr
 290 295 300
 Asn Glu Leu Leu Lys Ser Glu Gln Leu Leu Thr Ala Ser Glu Arg Asn
 305 310 315 320
 Leu Asp Phe Arg Asp Leu Tyr Asp Pro Arg Asp Lys Ala Lys Leu Leu
 325 330 335
 Tyr Asn Asn Leu Asp Ala Phe Gly Ile Met Asp Tyr Thr Leu Thr Gly
 340 345 350
 Lys Val Glu Asp Asn His Asp Asp Thr Asn Arg Ile Ile Thr Val Tyr
 355 360 365
 Met Gly Lys Arg Pro Glu Gly Glu Asn Ala Ser Tyr His Leu Ala Tyr
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 Arg Tyr Thr Gly Thr Pro Ile Pro Asp Asn Pro Asn Asp Lys
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 <212> DNA
 <213> Homo sapiens

<220>
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 agc aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa 96
 Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln
 20 25 30
 cag tgg gag cgg acc tac cta ggt aat gtg ttg gtt tgt act tgt tat 144
 Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys Thr Cys Tyr
 35 40 45
 gga gga agc cga ggt ttt aac tgc gaa agt aaa cct gaa gct gaa gag 192
 Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu
 50 55 60

act tgc ttt gac aag tac act ggg aac act tac cga gtg ggt gac act	240
Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr	
65 70 75 80	
tat gag cgt cct aaa gac tcc atg atc tgg gac tgt acc tgc atc ggg	288
Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly	
85 90 95	
gct ggg cga ggg aga ata agc tgt acc atc gca aac cgc tgc cat gaa	336
Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu	
100 105 110	
ggg ggt cag tcc tac aag att ggt gac acc tgg agg aga cca cat gag	384
Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu	
115 120 125	
act ggt ggt tac atg tta gag tgt gtg tgt ctt ggt aat gga aaa gga	432
Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly	
130 135 140	
gaa tgg acc tgc aag ccc ata gct gag aag tgt ttt gat cat gct gct	480
Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala	
145 150 155 160	
ggg act tcc tat gtg gtc gga gaa acg tgg gag aag ccc tac caa ggc	528
Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly	
165 170 175	
tgg atg atg gta gat tgt act tgc ctg gga gaa ggc agc gga cgc atc	576
Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile	
180 185 190	
act tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc	624
Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser	
195 200 205	
tat aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg	672
Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu	
210 215 220	
ctc cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag	720
Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu	
225 230 235 240	
agg cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc	768
Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr	
245 250 255	
gat gtt cgt	777
Asp Val Arg	

<210> 4

<211> 259

<212> PRT

<213> Homo sapiens

<400> 4

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1 5 10 15
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20 25 30
Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys Thr Cys Tyr
35 40 45
Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu
50 55 60
Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr
65 70 75 80
Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly
85 90 95
Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu
100 105 110
Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu
115 120 125
Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly
130 135 140
Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala
145 150 155 160
Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly
165 170 175
Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile
180 185 190
Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser
195 200 205
Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu
210 215 220
Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu
225 230 235 240
Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr
245 250 255
Asp Val Arg

<210> 5

<211> 1377

<212> DNA

<213> Streptococcus equisimilis

<400> 5

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agatatacca tgattgctgg acctgagtggt ctgctagacc gtccatctgt caacaacagc 180
caattgggtt ttagcggttg tggtactggt gaggggacga atcaagacat tagtcttaaa 240
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caagaattac tagctcaagc acaaagcatt ttaaacaata accaccagc ctatacgatt 780
tatgaacgtg actcctcaat cgtcactcat gacaatgaca ttttccgtac gattttacca 840
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tacaacaatc	tcgatgcttt	tggtattatg	gactatacct	taactggaaa	agtagaggat	1200
aatcacgatg	acaccaaccg	tatcataacc	gtttatatgg	gcaagcgacc	cgaaggagag	1260
aatgctagct	atcatttagc	ctatgataaa	gatcgttata	ccgaagaaga	acgagaagtt	1320
tacagctacc	tgcgttatac	agggacacct	atacctgata	accctaacga	caaataa	1377

<210> 6

<211> 1327

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 6

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aaataacagc	caattggttg	ttagcgttgc	tggtactgtt	gaggggacga	atcaagacat	180
tagtcttaaa	ttttttgaaa	tcgatctaac	atcacgacct	gctcatggag	gaaagacaga	240
gcaaggctta	agtccaaaat	caaaaccatt	tgctactgat	agtggcgcg	tgtcacataa	300
acttgagaaa	gctgacttac	taaaggctat	tcaagaacaa	ttgatcgcta	acgtccacag	360
taacgacgac	tactttgagg	tcattgattt	tgcaagcgat	gcaaccatta	ctgatcgaaa	420
cggcaaggtc	tactttgctg	acaaagatgg	ttcggttaacc	ttgccgaccc	aacctgtcca	480
agaatttttg	ctaagcggac	atgtgcgcgt	tagaccatat	aaagaaaaac	caatacaaaa	540
ccaagcgaaa	tctgttgatg	tggaatatac	tgtacagttt	actcccttaa	accctgatga	600
cgatttcaga	ccaggtctca	aagatactaa	gctattgaaa	acactagcta	tcggtgacac	660
catcacatct	caagaattac	tagctcaagc	acaaagcatt	ttaaacaaaa	accacccagg	720
ctatacgatt	tatgaacgtg	actcctcaat	cgtcactcat	gacaatgaca	ttttccgtac	780
gattttacca	atggatcaag	agtttactta	ccgtgttaaa	aatcgggaac	aagcttatag	840
gatcaataaa	aaatctggtc	tgaatgaaga	aataaacaac	actgacctga	tctctgagaa	900
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cttaacagct	agcgaacgta	acttagactt	cagagattta	tacgatcctc	gtgataaggc	1080
taaactactc	tacaacaatc	tcgatgcttt	tggtattatg	gactatacct	taactggaaa	1140
agtagaggat	aatcacgatg	acaccaaccg	tatcataacc	gtttatatgg	gcaagcgacc	1200
cgaaggagag	aatgctagct	atcatttagc	ctatgataaa	gatcgttata	ccgaagaaga	1260
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caaataa						1327

<210> 7

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<221> CDS

<222> (2)...(52)

<400> 7

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	Asn	Ala	Ser	Tyr	His	Leu	Ala	Gly	Gly	Gly	Gln	Ala	Gln	Gln	Ile	Val	
1					5					10						15	

ccc
Pro

52

<210> 8
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 8
Asn Ala Ser Tyr His Leu Ala Gly Gly Gly Gln Ala Gln Gln Ile Val
1 5 10 15
Pro

<210> 9
<211> 1541
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 9
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atcaagacat tagtcttaaa ttttttgaaa tcgatctaac atcacgacct gctcatggag 180
gaaagacaga gcaaggctta agtcctaaaat caaaaccatt tgctactgat agtggcgcgga 240
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aacctgtcca agaatttttg ctaagcggac atgtgcgctg tagaccatat aaagaaaaac 480
caatacaaaa ccaagcgaaa tctgttgatg tggaatatac tgtacagttt actcccttaa 540
accctgatga cgatttcaga ccagggtctca aagatactaa gctattgaaa aactagcta 600
tcggtgacac catcacatct caagaattac tagctcaagc acaaagcatt ttaaacaanaa 660
accacccagg ctatacgatt tatgaacgtg actcctcaat cgtcactcat gacaatgaca 720
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ccacatcgag cggatctggc cccttcaccg atgttcgtta g 1541

<210> 10
<211> 1661

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

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tgattgctgg acctgagtgg ctgctagacc gtccatctgt caacaacagc caattgggtg 240
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taaaggctat tcaagaacaa ttgatcgcta acgtccacag taacgacgac tactttgagg 480
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cttaccgagt ggggtgacct tatgagcgct ctaaagactc catgatctgg gactgtacct 1620
gcatcggggc tgggcgaggg agaataagct gtaccatcta a 1661

<210> 11
<211> 1782
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 11
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acgctgccc agatctcgat cccgcgaaat taatacgact cactataggg agaccacaac 180
ggtttccctc tagaaataat tttgtttaac tttagaagg agatatacca tgggtgcaagc 240
acaacagatt gtacccatag ctgagaagtg ttttgatcat gctgctggga cttcctatgt 300
ggtcggagaa acgtgggaga aggcagcgga cgcactactt gcacttctag aaatagatgc 360
aacgatcagg acacaaggac atcctataga attggagaca cctggagcaa gaaggataat 420
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ttagcctatg	ataaagatcg	ttataccgaa	gaagaacgag	aagtttacag	ctacctgcgt	1740
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<210> 12

<211> 2096

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 12

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atcaggacac	aaggacatcc	tatagaattg	gagacacctg	gagcaagaag	gataatcgag	1980
gaaacctgct	ccagtgcac	tcacacaggca	acggccgagg	agagtggaag	tgtgagaggc	2040
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<210> 13
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetically generated primer

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		53

<210> 14
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetically generated primer

<400> 14		
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<210> 15
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetically generated primer

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetically generated primer

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<210> 17
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 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetically generated primer

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43

<210> 18

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 18

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52

<210> 19

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 19

gtacggatcc gaatgctagc tatcatttag cgggtggtgg tcaggcgag caaatggtt

59

<210> 20

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 20

ggccttaaga gcgctctatt agatgttaca gcttattct

39

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 21

ccatggtgca agcacaacag attgtacca tagctgagaa gtgt

44

<210> 22

<211> 40

<212> DNA

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<220>
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27
